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Translation of the amended claims

1. Method for detecting a nucleotide sequence in a nucleic acid molecule comprising the following steps:
   (a) hybridization of nucleic acid molecules to a set of probes of different nucleobase sequences, wherein each probe has a mass that differs from the one of all the other probes;
   (b) separation of the probes that were not hybridized;
   (c) detachment of a specifically hybridized probe in a solvent;
   (d) analysis of the hybridized probes in a solution by means of electrospray mass spectrometry; and
   (e) determination of the nucleic acid molecules by means of the probes hybridized to them.

2. Method according to claim 1, wherein the nucleic acid molecules are immobilized at the surface of a support before or after step (a).

3. Method according to claim 2, wherein the immobilization of the nucleic acid molecules at the surface is carried out via an NH_2, epoxy or SH function by means of coating the surface of the probe supports with a silicate or silane, via a protein-substrate, protein-protein or a protein-nucleic acid interaction or via an interaction of two hydrophobic buiiiding blocks.

4. Method according to claim 3, wherein the protein-substrate interaction is a biotin-streptavidin bond or an antibody-antigen bond.

5. Method according to claim 3, wherein the protein-nucleic acid interaction is a Gene32-nucleic acid bond.

6. Method according to any one of claims 1 to 5, wherein the probes are nucleic acids having a mass tag.

7. Method according to claim 6, wherein the mass tag is at the same time a charge tag.

8. Method according to claim 6, wherein the nucleic acids moreover have a charge tag.

9. Method according to any one of claims 1 to 8, wherein the probes are modified nucleic acid molecules.

10. Method according to claim 9, wherein the modified nucleic acid molecules are PNAs, alkylated phosphorothioate nucleic acids or alkylphosphonate nucleic acids.

11. Method according to any one of claims 1 to 10, wherein the probes are generated by means of combinatorial solid phase synthesis.

12. Method according to claim 11, wherein different base builiding blocks are labelled in such a way that the probes synthesized therefrom can be differentiated in the mass spectrometer due to their mass.

13. Method according to claim 12, wherein the labelling is a methyl, ethyl, propyl, a branched or non-branched alkyl, a halogen substituted branched or non-branched alkyl, alkoxyalkyl, alkylaryl, arylalkyl, alkoxyaryl or aryloxyalkyl group or one of their deuterated or other isotopic variants.

14. Method according to any one of claims 10 to 13, wherein the probes have at least one modification in a defined position away from randomized nucleotides allowing for the cleavage of the probe.

15. Method according to claim 14, wherein modification means the introduction of a phosphorothioate group and/or an RNA base and/or a phosphotriester bond into the probe.

16. Method according to any one of claims 1 to 15, wherein the probes are generated as partial libraries having different mass and/or charge tags.

17. Method according to any one of claims 1 to 16, wherein the positions of the probes on the probe support allow for an allocation to the nucleic acid molecules hybridizing thereto.

18. Kit comprising
    (a) a set of probes as defined in any one of claims 6 to 16 and/or
    (b) a probe support which has been pretreated and thus allows for the attachment of target DNAs and/or target DNAs that have already been attached.